CGG GCG ACC AGC GAC CAT GGA TCA ည္ဟ ATG 1 GAT TTT TTG TGA TAT CTT CTG GGG GGG GGG GAA CCT ATT GTA TAA ACG CCA ACC AAC TTG AAA GGG AAG TAC CCA AGC CGC CTC TCG CCG GCG CGT TGT GCG ATT CAT TAA TAC AGC TGC CAC ACA ATT AAT GTG AGT TAG CTC ACT GTG AGC သည ATC ď TTCTAA $^{\mathrm{TGG}}$ 505 550 GTT CCT GGA AGG GGA CCG ACC CCC AGC GAT TCA TGG AGC GAG GAA AGC AAT TAG GGA ATT TAC GTC CAA GCT CGA AAT CCC CTG ATT CCT TGT GGG ATA ACC CGT ATT CCC CCC CTT AGA GTG GCT CCA GGA ATT CGC CAC GAC CGG GAG GAC CGA GGA GGC GCC AGA CTA TAG AAC TGG TAA AAT TTG TGT CGG CCG CIC TIT AIG CIT CCG GCT CGT AIG TTT GGC CCA AGT GAG CGC AAC CAT GAT AAG GGA ACA AAA ACT GGA GCT CCA CCG CGG TGG TTA CTT TAT GAC TTT GGG TAC CTG GCC ATT GCG GTC TAA CAA TTT CAC ACA GGA AAC AGC CAC AAA TTA $^{
m TGG}$ CAG GCT CCC GAC သသ 379 TAG GCA CCC TTTATC TCG CAA TTT64 CCC 127 TTA CTTCCC 316 AGG 568 CGG 190 253 442

TTC

Asn Leu

Asp Leu

AAT

TTG

GAC

GGG TAT GIY TYR

TGG CCA G

ATG GAT GAT MET ASP 1

ATT Ile

Val GTC

Pro

GTG Val

CGC G1y

CCT

CGC Arg

ACC Thr

929

629

AGC

DSSCINE OF ACC.

- GTG Val ATT Ile ATC GlyGGT CAT His Pro CCT Ile ATC CTC Val GTC TyrTAT G1u GAG Leu TTG Asp GAC GlyGGA $\frac{\mathtt{TAT}}{\mathtt{TY}r}$ TAT His CAC Gln CAG Pro CCA TAC ACG 692
- GTC Val ATG Ile ATC GAC Asp AGT Ser TAT $\frac{GGA}{G1Y}$ ATA Ile GAC AAA Lys ATG MET ATT Ile GAT Asp AAG GCC Ala CTG Leu 550 Arg GAG Glu ATT Ile AGA Arg GAC 755
- ATC Ile AAC Asn AAG Lys CTT Leu CAC His Glu GAA GTA Val CTC GAT Asp GCT TGT CysTTC Phe AAA Lys $\frac{\text{TAC}}{\text{TY} r}$ GGG G1y GGG G1y $\frac{AAA}{Lys}$ Leu CLL GTG Val $_{\mathrm{TGT}}$ Cys CTG818
- AGG Arg TAC Tyr AGT Ser AAA Lys CTA Leu AGA Arg ATC Ile TTC Phe Asp GAT GTT Val Lys AAG ATG MET TCA Ser GTC Val Phe TTT CGG Arg Asp GAT Ser TCA AAT Asn CGA Arg AGC Ser 881
- GGA GlyGCT Ala CTG Leu ACG Thr Ser TCA CTT Leu GAT Asp $\frac{\text{GGT}}{\text{Gl}\, \text{y}}$ GGC GlyGlyGGA IleATC ATA IleGln CAG ATG MET GAG Glu GGT GlyATG MET TCC Ser Gln CAG Asp GAC AAT 944
- AGC Ser CTC Leu CTA GCA Ala AAA Lys MET ATG ACC AGG Arg $\frac{\mathsf{GGG}}{\mathsf{Gl}\,\mathtt{y}}$ ACT $\frac{\text{GGA}}{\text{Gly}}$ GTC Val GTT Val GAT GAG Glu Val GIT ATT Ile Len CIC TTT Asn AAT AAG Lys 1007
- TCC ACA Thr AGA Arg AAG GTG Val TTG Leu TTG AGT Ser GCC Ala GTA Val AAG Lys ATT Ile ATG <u>AAC</u> Asn CCC Pro AAG Lys TAC AAA LysGAG Glu ATA I1eAAT 1070
- GGA Gly GIG Val GTG Val Phe TTT TTA CAC CCA Ile ATT GAG TTT Phe GGA G1yGCT Ala $\frac{\mathtt{TAT}}{\mathtt{TYr}}$ GAC Asp Pro CCT Arg AGA Phe TTT GlyGGC GAC Asp AGT Ser AGA 1133

FIG. 1B

COSCEZCE CZIECI

TAT GCC TTA GAT TAC AAT GAA TAC TTC AGA GAT CTG AAT CAC ATA TGC GTC ATC AAT GAG CAC TYR Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile Asn Glu His 1196

 $\overline{ ext{TAA}}$ AGG AAA ATA TCG AGT CTT AAA GAC ATG AAT TCT CAC CAC TAA AGG CCC CAG ATA GGA STP GGG Gly 1259

1322 TCA TTT TTA CGC CTG TCT TGG GGA GCC AGT TGC AAG TTG GGC CCC CCC GGA TCT TCA TCA GGA

1385 GG

FIG. 1C

1	MATRSPGVVISDDEPGYDLDLFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKE	56
1		56
57	MGGHHIVALCVLKGGYKFFADLLDYIKALNRNSDRSIPMTVDFIRLKSYCNDQSTG	112
57	: . :.	112
113	DIKVIGGDDLSTLTGKNVLIVEDIIDTGKTMQTLLSLVRQYNPKMVKVASLLVKRT	168
110		
113	EMQIIGGGDLSTLAGKNFLIVEDVVGTGRTMKALLSNIEKYKPNMIKVASLLVKRT	168
169	PRSVGYKPDFVGFEIPDKFVVGYALDYNEYFRDLNHVCVISETGKAKYKA	218
169	SRSDGFRPDYAGFEIPHLFVVGYALDYNEYFRDLNHICVINEHG*RKISS	218

FIG.2

20 30 30	P H G V I M D R I E R L A 50 P H G I I V D R I E R L A P H G L I M D R T E R L A P H G V I M D R T E R L A P N G V I K N R I E K L A P R G V A Q R I A D D Y S N K G G Y K F F A D L L D H	L C V L K G G Y K F C A D L V E H L HPRT2b.pep L C V L K G G Y K F F A D L L D Y I HPRThu L C V L K G G Y K F F A D L L D Y I HPRTcl L C L L K G S R G F F T A L L K H L HPRTplas V S V L K G S F V F T A D M V R I L HPRTtyrnan
TRS-PGV 10 TRS-PGV TRS-PGV TRS-PSV IPNNPGAGENA PACK	23 T Y P Q H Y Y G D L E K V L I P 23 T Y P Q H Y Y G D L E Y V L I P 23 C I P N H Y A E D L E K V F I P 31 M I P A H Y K K Y L T K V L V P 10 A T S V L F T E A E L H T R M - V M K E M G G H H I V A L C V L 70	M V L C V A L C V A L C V A L C V V A L C V V V V V V V V V V V V V V V V V V

FIG.3A

Majority O HPRT2b.pep HPRThu HPRTcl HPRTplas	Majority HPRT2b.pep HPRTcl HPRTcl HPRTplas	Majorıty HPRT2b.pep HPRThu HPRTcl HPRTplas HPRTtrypan
PMTV DFIRLKSYCND 0 110 110 120 MKV DFIRLKSYRND 0 MTV DFIRLKSYCND 0 MTV DFIRLKSYCND 0 KPLFGEHYVRVKSYCND 0	V E D I I D T 150 V E D V V G T V E D I I D T V E D I I D T V E D I I D T V E D I I D T	_
DFIRLKSY 110 DFIRLKSY DFIRLKSY GEHYVRVKSY GEHYVRVKSY	S M G E M Q I I G G D D L S T L T G K N V L I V E D I I D 130 140 140 1 A S T G D I K V I G G D D L S T L A 3 K N F L I V E D V V G S T G D I K V I G G D D L S T L T G K N V L I V E D I I D S T G T L E I V S - E D L S C L K G K H V L I V E D I I D K S C G R V D V K A D G L C D I R G K H V L V L E D I I D	G R T M K A L L S L V K K Y E P K M V K V A S L L V K R T S 160 170 180 G K T M Q T L L S L V R Q Y N P K M V K V A S L L V K R T P G K T M Q T L L S L V R Q Y N P K M V K V A S L L V K R T P G K T L V K F C E Y L K R F F I K T W A I A C F I K R T P A L I L R E V V D S L K K S E P A S I K T L V A I D K P G G
SDRSVPMTV 100 SDRFWSMKW SDRSIPMTV SDRSIPMTV SAVEMSKPLFGE	G D D L S T L G D D L S T L G D D L S T L C D D L S T L C D L S T L C D L S T L C D L S C D D L S C D D L S C D D L S C D D L S C D D C D D C D D C D D D D C D D D D C D D D D C D D D D C D D D D C D D D D C D D D D C D D D D C D	160 N I E K Y K P N L V R Q V N P K L V K R Y N P K Y L K K F F I I K S L K K S F P A
KALNRNSDRSVPMT 100 KALNRNSDRFWSMK KALNRNSDRSIPMT KALNRNSDRSIPMT SRIHNYSAVEMSKP GDFGVPTR	GEMQIG GDIKVIG GDIKVIG GTLEIVS CGRVDVK	1
83 K A 83 K A 84	110 S M 110 S T 110 S T 121 S T 89 K S	140 G R T 140 G K T 140 G K T N 140 G K T N 150 G K T N 119 A L T L

FIG.3B

R S V G F K P D F V G F E I P D K F V V G Y A L D Y N E Y F Majority R S D G F R P D Y A G F E I P H L F V V G Y A L D Y N E Y F HPRT2b.pep R S V G Y K P D F V G F E I P D K F V V G Y A L D Y N E Y F HPRTcl W N G F K A D F V G F E I P D K F V V G Y S L D Y N E Y F HPRTcl R X I P F T A E Y W V A D V P N V F V V G Y G L D Y D Q S Y HPRTtrypan	R D L N H V C V I S E T G K A K Y K A Majority R D L N H I C V I N E T G K A K Y K A HPRT2.pep R D L N H I C V I S E T G K A K Y K A HPRThu R D L D H C C L V N E T G K K Y K A HPRTc1 R E V R D W V I L K P S V Y E T W G K E L E R R A A G E A HPRTtrypan	Majority HPRT2b.pep HPRTcl HPRTcl HPRTcl HPRTplas
170 R S D 170 R S V 170 R S V 170 R S V 180 L W N 149 R K I P	200 R D L N 200 R D L N 200 R D L N 210 R D L D 179 R E V R	212 218 218 231 L 209 K R

FIG.3C

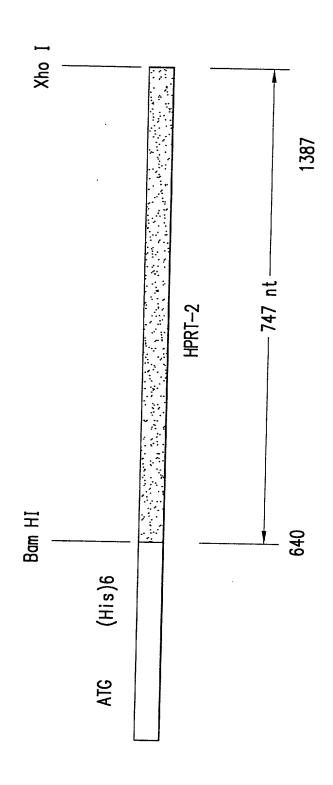


FIG.4

